

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:25:32 ; Search time 5.66667 Seconds  
(without alignments)  
91.287 Million cell updates/sec

Title: US-09-743-225-4  
Perfect score: 62  
Sequence: 1 RDKATFGFHGDG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	56	90.3	345	1	APOH_HUMAN	P02749 homo sapien
2	46	74.2	345	1	APOH_MOUSE	Q01339 mus musculus
3	42	67.7	1310	1	Y335_SCHPO	Q14340 schizosaccharomyces pombe
4	41	66.1	297	1	APOH_RAT	P26644 rattus norvegicus
5	41	66.1	345	1	APOH_CANFA	P33703 canis familiaris
6	40	64.5	345	1	APOH_BOVIN	P17690 bos taurus
7	40	64.5	363	1	DPB8_SPICI	P34029 spiroplasma
8	38	61.3	283	1	FL123_COREV	074631 coriolus ve
9	37	59.7	537	1	DEXB_STREQ	059905 streptococcus
10	36	58.1	307	1	Y650_VIBCH	Q9ku39 vibrio cholerae
11	36	58.1	417	1	TRMU_YEAST	Q12093 saccharomyces cerevisiae
12	36	58.1	477	1	FIBB_PETRA	P02678 petromyzon marinus
13	36	58.1	496	1	CWBL_BACSU	Q02114 bacillus subtilis
14	36	58.1	798	1	PHEG_BACSU	P39123 bacillus subtilis
15	36	58.1	964	1	UL70_MCMVS	Q69153 murine cytomegalovirus
16	35	56.5	198	1	IFP2_ARATH	Q04663 arabidopsis thaliana
17	35	56.5	241	1	PYRH_HAUNI	Q9hn88 halobacteri
18	35	56.5	574	1	SYR_BUCAI	Q44683 buchnera apiculata
19	35	56.5	962	1	UL52_PRVKA	Q85228 pseudoradulara
20	35	56.5	2209	1	KNTC_HUMAN	P50748 homo sapiens
21	34	54.8	151	1	GLBB_CHITTH	P02227 chironomus
22	34	54.8	162	1	GLB6_CHITTH	P02224 chironomus
23	34	54.8	366	1	QUBA_CADCR	Q9a7y2 caulobacter
24	34	54.8	373	1	YSAK_CAEEL	Q93454 caenorhabditis elegans
25	34	54.8	398	1	CGL_MOUSE	Q8vcn5 mus musculus
26	34	54.8	415	1	RF11_METAC	P02226 methanococcus
27	34	54.8	418	1	YML13_YEAST	Q04526 saccharomyces cerevisiae
28	34	54.8	644	1	XIND_CELL1	P54865 cellulosimicrobium
29	34	54.8	699	1	MALO_HAZIN	P45176 haemophilus ducreyi
30	34	54.8	937	1	SYL_ECOLI	P00956 escherichia coli
31	34	54.8	973	1	DYRA_RHIME	P56899 rhizobium m
32	33	53.2	145	1	GLB7_CHITTH	P02226 chironomus
33	33	53.2	161	1	GLB9_CHITTH	P02223 chironomus

#### ALIGNMENTS

34	33	53.2	162	1	GLBH_CHITH	P12550 chironomus
35	33	53.2	162	1	GLBH_CHITP	P29242 chironomus
36	33	53.2	349	1	ALFL_CHLPN	Q9z8q7 chlamydia pneumoniae
37	33	53.2	398	1	TRMU_BRDME	Q8y116 brucella melitensis
38	33	53.2	430	1	MAS1_JGRT9	P50202 agrobacteri
39	33	53.2	475	1	EX1_ECOLI	P04995 escherichia coli
40	33	53.2	505	1	SM1_YEAST	P52911 saccharomyces cerevisiae
41	33	53.2	562	1	ERX2_YEAST	P26309 saccharomyces
42	33	53.2	610	1	CC20_YEAST	P26309 saccharomyces
43	33	53.2	713	1	CDG2_PAEM	P26309 saccharomyces
44	33	53.2	921	1	SVT_BACSU	P45477 bacillus subtilis
45	33	53.2	923	1	AGLU_TETPY	P00906 tetrahymena

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35	33					

- Int. Immunol. 3:1217-1221(1991).  
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- SEQUENCE FROM N.A.; PubMed=914524;  
 RX MEDLINE=99115472; Rasmussen T.E., Sanghera D.K., Kamboh M.I., Kristensen T.;  
 Okkels H., Structure of the human beta2-glycoprotein I (apolipoprotein H) gene.;  
 Eur. J. Biochem. 259:435-440(1999).  
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- SEQUENCE FROM N.A.;  
 TISSUE=Liver;  
 RC MEDLINE=22388257; PubMed=12477932;
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- SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
 RX MEDLINE=84122015; PubMed=6587378;
- Rozier J., Takabashi N., Putnam F.W., "Compete amino acid sequence of human plasma beta 2-glycoprotein I.": Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
- SEQUENCE OF 20-348.  
 RX MEDLINE=93050249; PubMed=1426288;
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- DISULFIDE BONDS IN C-TERMINAL DOMAIN.  
 RX MEDLINE=93050249; PubMed=1426288;
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- STRUCTURE OF CARBOHYDRATES.  
 RX MEDLINE=9739994; PubMed=155091;
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 [12]
- X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RX MEDLINE=99437994; PubMed=10508150;
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 [13]
- X-RAY CRYSTALLOGRAPHY (2.87 ANGSTROMS).  
 RX MEDLINE=20031634; PubMed=10562535;

- RA Schwarzenbacher R., Zeth K., Diederichs K., Gries A., Kostner G.M., Lagner P., Pressl R.; "Crystal structure of human beta2-glycoprotein I: implications for phospholipid binding and the antiphospholipid syndrome.": RT  
 RA MEDLINE=99123313; PubMed=8099061;  
 RA "Human beta 2-glycoprotein I: molecular analysis of DNA and amino acid polymorphism"; RT  
 RA VARIANT LEU-266; RT  
 RA MEDLINE=93273313; PubMed=9225969;  
 RA "Molecular basis of the apolipoprotein H (beta 2-glycoprotein I) protein polymorphism"; RT  
 RA Hum. Genet. 91:401-402(1993).  
 RN [14]
- RA VARIANT ASN-107; RP  
 RA MEDLINE=9739481; PubMed=9063752;  
 RA Sanghera D.K., Kristensen T., Hammann R.P., Kamboh M.I.; RT  
 RA "Identification of structural mutations in the fifth domain of apolipoprotein H (beta-2-glycoprotein I) which affect phospholipid binding.": RT  
 RA Hum. Mol. Genet. 6:311-316(1997).  
 RN [15]
- RA VARIANTS GLY-325 AND SER-335; RP  
 RA MEDLINE=9721779; PubMed=9063752;  
 RA Sanghera D.K., Wagenknecht D.R., RT  
 RA "Activation of the intrinsic blood coagulation cascade by binding substances such as heparin, phospholipids, and dextran sulfate may prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells.": RT  
 RA Hum. Mol. Genet. 6:311-316(1997).  
 RN [16]
- CC 1-- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.  
 CC 1-- SUBCELLULAR LOCATION: Secreted.  
 CC 1-- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC 1-- SIMILARITY: Contains 4 Sushi (SCR) domains.  
 CC 1--  
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 CC 1--  
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 CC 1--  
 DR EMBL; X53595; CAA37664.1; DR EMBL; X53595; CAA37664.1;  
 DR EMBL; Y57847; CRA40977.1; DR EMBL; Y57847; CRA40977.1;  
 DR EMBL; M62839; AAA51766.1; DR EMBL; M62839; AAA51766.1;  
 DR EMBL; S80305; AAB21330.1; DR EMBL; Y11493; CRA72279.1;  
 DR EMBL; Y11494; CRA72279.1; DR EMBL; Y11494; CRA72279.1;  
 DR EMBL; Y11495; CRA72279.1; DR EMBL; Y11495; CRA72279.1;  
 DR EMBL; X53595; CRA72279.1; DR EMBL; X53595; CRA72279.1;  
 DR EMBL; Y11496; CRA72279.1; DR EMBL; Y11496; CRA72279.1;  
 DR EMBL; Y11497; CRA72279.1; DR EMBL; Y11497; CRA72279.1;  
 DR EMBL; Y17754; CRA76845.1; DR EMBL; Y17754; CRA76845.1;  
 DR EMBL; BC026283; AAH26283.1; DR EMBL; BC026283; AAH26283.1;  
 DR PIR; S17178; NBNU; DR PIR; S17178; NBNU;  
 DR IQUB; 08-OCT-99; DR PDB; 1C1Z; 19-NOV-99;  
 DR PDB; 1G4F; 28-MAR-01; DR PDB; 1G4G; 28-MAR-01;  
 DR SMART; SM00032; CCP; 4; DR Genew; HGNC:616; APOH.  
 DR MM; 138700; DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00084; sushi\_4; DR Heparin-binding Glycoprotein; Plasma; Repeat; Sushi; Signal;  
 DR KW Polymorphism; 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 345  
 FT DOMAIN 22 80  
 RX BETA-2-GLYCOPROTEIN I.  
 RX SUSHI 1.



RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;	-	
RL	"The genome sequence of Schizosaccharomyces pombe.";		
CC	Nature 415:671-680(2002).		
CC	-I- SIMILARITY: BELONGS TO THE OSBP FAMILY.		
CC	-I- SIMILARITY: Contains 1 PH domain.		
CC	-I- SIMILARITY: Contains 3 ANK repeats.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).		
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CC	EMLB: Z97211; CAB10154.2; -.		
DR	PIR: T40135; T40135.		
DR	GeneDB_Spondie; SPBC2P12; 05c; -.		
DR	InterPro: IPR000110; ANK.		
DR	InterPro: IPR000648; Oxysterol_BP.		
DR	InterPro: IPR000849; PH.		
DR	Pfam: PF00023; ankyrin repeat.		
DR	Pfam: PF01237; Oxysterol_BP; 1.		
DR	Pfam: PF00169; PH; 1.		
DR	SMART: SM00248; ANK; 3.		
DR	SMART: SM00233; PH; 1.		
DR	PROSITE; PS50080; ANK_REPEAT; 2.		
DR	PROSITE; PS50298; ANK REP REGION; 1.		
DR	PROSITE; PS01013; OSBP; FALSE NEG.		
DR	PROSITE; PS50005; PH_DOMAIN; 1.		
KW	Hypothetical protein; Lipid transport; transport; ANK repeat; Repeat.		
FT	REPEAT 54 84 ANK 1.		
FT	REPEAT 88 118 ANK 2.		
FT	REPEAT 188 217 ANK 3.		
FT	DOMAIN 254 349 PH.		
SEQ	SEQUENCE 1310 AA; 148474 MW; E6F284F09C073262 CRC64;		
Query Match Score 42; DB 1; Length 1310; Best Local Similarity 67.7%; Pred. No. 3.1; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy	2 DKATGFHD 10	Query Match Score 41; DB 1; Length 297; Best Local Similarity 70.0%; Pred. No. 1; Mismatches 1; Indels 0; Gaps 0;	
Db	362 DNATGFHD 370		
<b>RESULT 4</b>			
APOR_RAT	STANDARD; PRT; 297 AA.		
AC	P26644;		
DT	01-AUG-1992 (Rel. 23, Created)		
DT	01-FEB-2003 (Rel. 41, Last sequence update)		
DE	Beta-2' glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)		
GN	APOH.		
OS	Rattus norvegicus (Rat).		
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.		
OX	NCBI_TaxID-10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Sprague-Dawley;		
RX	MSDLIN=8936680; PubMed=2771654;		
RA	Aoyama Y.; Chan Y.L.; Woo I.G.		
RT	"The primary structure of rat beta 2'-glycoprotein I."		
RL	"The primary structure of rat beta 2'-glycoprotein I."		
CC	-I- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE, MAY PREVENT ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING		
CC	-I- SUBCELLULAR LOCATION: Secreted.		
CC	-I- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.		
<b>RESULT 5</b>			
APOR_CANFA	STANDARD; PRT; 345 AA.		
ID	APOR_CANFA		
AC	P3703;		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Beta-2' glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)		
DE	Beta-2' glycoprotein I Precursor (Apolipoprotein H) (Apo-H) (B2GPI)		
GN	APOR.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID-9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Beagle; TISSUE-Liver;		
RX	MEDLINE=9321500; PubMed=1682067;		
RA	Sellar G.C., Keane J., Mahdi H., Peeples M.E., Browne N., Whitehead A.S.;		
RA	"Characterization and acute phase modulation of canine apolipoprotein H (beta 2-glycoprotein I)."		
RT	Biochem. Biophys. Res. Commun. 191:1288-1293(1993).		
RL	-I- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES		

CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT  
 CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING  
 CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC -|- SIMILARITY: Contains 4 Sushi (SCR) domains.

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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [licensing@isb-sib.ch](mailto:licensing@isb-sib.ch)).  
 CC

CC EMBL; X72933; CAA51438.1; -.  
 DR PIR; JN0465; JN0465.  
 DR HSSP; P02749; 1C1Z.  
 DR InterPro; IPR00446; Sushi\_SCR\_CCP.  
 DR Pfam; PF0008A; sushi; 4.  
 DR SMART; SM00032; CCP; 4.  
 RW Rehein-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.  
 FT SIGNAL\_1 19 BY SIMILARITY.  
 FT CHAIN 20 345 BEPA-2-GLYCOPROTEIN I.  
 FT DOMAIN 22 80 SUSHI 1.  
 FT DOMAIN 83 138 SUSHI 2.  
 FT DOMAIN 141 201 SUSHI 3.  
 FT DOMAIN 263 345 SUSHI 4.  
 FT DISULFID 23 66 BY SIMILARITY.  
 FT DISULFID 51 79 BY SIMILARITY.  
 FT DISULFID 84 124 BY SIMILARITY.  
 FT DISULFID 110 137 BY SIMILARITY.  
 FT DISULFID 142 188 BY SIMILARITY.  
 FT DISULFID 174 200 BY SIMILARITY.  
 FT DISULFID 205 248 BY SIMILARITY.  
 FT DISULFID 234 260 BY SIMILARITY.  
 FT DISULFID 264 315 BY SIMILARITY.  
 FT DISULFID 300 325 BY SIMILARITY.  
 FT DISULFID 307 345 BY SIMILARITY.  
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 345 AA; 3803 MW; E0B2624879B/4FEA CRC64;

Query Match 66.1%; Score 41; DB 1; Length 345;  
 Best Local Similarity 70.0%; Pred. No. 1.2;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KDKAFTGHD 10  
 DB 227 KDKAMYGCHD 236

RESULT 6  
 AP0H\_BOVIN AP0H\_BOVIN STANDARD; PRT; 345 AA.  
 ID AP0H\_BOVIN P17630; Q28052;  
 AC 01-ARG-1990 (Rel. 15, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)  
 DE (Beta(2)GPI).  
 GN APOH.  
 OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Eukaryota; Metazoa; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 NCBI\_TAXID=9913;  
 [1] RN SEQUENCE FROM N.A.  
 RP

RA TISSUE-Liver; Gao B.; Vielman M.; Romm E.; Lazar-Wesley E.; Sakauchi K.,  
 RA Appella E.; Kunos G.; Takacs I.; Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE OF 4-345 FROM N.A.; PARTIAL SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE-Liver;  
 RX MEDLINE-92232647; PubMed=1567819;  
 RA Bendixen B.; Halkier T.; Magnusson S.; Sottrup-Jensen L.,  
 RA Kristensen T.;  
 RT "Complete primary structure of bovine beta 2-glycoprotein I: localization of the disulfide bridges.";  
 RT Biochemistry 31:3611-3617(1992).  
 RL [3]  
 RN SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
 RP TISSUE-Plasma;  
 RX MEDLINE-92089075; PubMed=1751487;  
 RA Kato H.; Enyoyaji K.-I.;  
 RT "Amino acid sequence and location of the disulfide bonds in bovine beta 2 glycoprotein I: the presence of five Sushi domains.";  
 RL Biochemistry 30:11687-11694(1991).  
 [4]  
 RN SEQUENCE OF 20-41.  
 RP MEDLINE-90226328; PubMed=2327984;  
 RX MEDLINE-90226328; PubMed=2327984;  
 RA L1 O.; Blacher R.; Esch F.; Conote L.P.;  
 RT "Isolation from fetal bovine serum of an apolipoprotein-H-like protein which inhibits thymidine incorporation in fetal calf erythroid cells.";  
 RL Biochem. J. 267:261-264(1990).  
 CC -|- FUNCTION: Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dextran sulfate. May prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC -|- SIMILARITY: Contains 4 Sushi (SCR) domains.  
 CC -|-  
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 CC -|-  
 CC EMBL; L07303; AAA30382.1; -.  
 DR EMBL; X60065; CA42669.1; -.  
 DR PIR; JN0502; NBBO.  
 DR HSSP; P02749; 1C1Z.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF0008A; sushi; 4.  
 DR SM00032; CCP; 4.  
 KW Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.  
 FT SIGNAL\_1 19 BY SIMILARITY.  
 FT CHAIN 20 345 BEPA-2-GLYCOPROTEIN I.  
 FT DOMAIN 22 80 SUSHI 1.  
 FT DOMAIN 83 138 SUSHI 2.  
 FT DOMAIN 141 201 SUSHI 3.  
 FT DOMAIN 263 345 SUSHI 4.  
 FT DISULFID 23 66 BY SIMILARITY.  
 FT DISULFID 51 79 BY SIMILARITY.  
 FT DISULFID 84 124 BY SIMILARITY.  
 FT DISULFID 110 137 BY SIMILARITY.  
 FT DISULFID 142 188 BY SIMILARITY.  
 FT DISULFID 174 200 BY SIMILARITY.  
 FT DISULFID 205 248 BY SIMILARITY.  
 FT DISULFID 234 260 BY SIMILARITY.  
 FT DISULFID 264 315 BY SIMILARITY.  
 FT DISULFID 300 325 BY SIMILARITY.  
 FT DISULFID 307 345 BY SIMILARITY.  
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 345 AA; 3803 MW; E0B2624879B/4FEA CRC64;

CARBOHYD	183	183	N-LINKED (GLCNAC. .).	
CARBONID	193	193	N-LINKED (GLCNAC. .).	
CARBONID	253	253	N-LINKED (GLCNAC. .).	
CONFLICT	101	101	E -> G (IN REF. 1).	
CONFLICT	108	108	S -> R (IN REF. 1).	
CONFLICT	177	177	H -> R (IN REF. 1).	
CONFLICT	191	191	H -> N (IN REF. 3).	
CONFLICT	194	194	W -> C (IN REF. 1).	
CONFLICT	259	259	S -> N (IN REF. 1).	
CONFLICT	302	302	H -> N (IN REF. 1).	
CONFLICT	305	305	K -> R (IN REF. 1).	
CONFLICT	329	329	H -> R (IN REF. 1).	
SEQUENCE	345 AA;	38252 MW;	E117DAB609461C33 CRC64;	
Query Match	64.5%	Score 40;	DB 1;	Length 345;
Best Local Similarity	70.0%	Pred. No.	1.9;	
Matches	7;	Conservative	1;	Mismatches .2;
				Indels 0;
				Gaps 0;
RESULT 7				
DP3B_SPICI	STANDARD;	PRT;	363 AA.	
P34029;	01-FEB-1994 (Rel. 28, Created)			
	01-FEB-1994 (Rel. 28, Last sequence update)			
	28-FEB-2003 (Rel. 41, Last annotation update)			
DNA polymerase III, beta chain	(EC 2.7.7.7).			
DNAN.				
Spiroplasma citri.				
Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;				
Spiroplasmataceae; Spiroplasma.				
[1]				
SEQUENCE FROM N.A.				
STRAIN=R842HP;				
MEDLINE=94290261;				
NCBI_TAXID=2133;				
[1]				
Ye F., Renaudin J., Bove J.M., Lairget F.;				
"Cloning and sequencing of the replication origin (oriC) of the				
Spiroplasma citri chromosome and construction of autonomously				
replicating artificial plasmids.";				
Curr. Microbiol. 29:23-29 (1994).				
-I- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME				
RESPONSIBLE FOR MOST OF THE REPLICATIVE ACTIVITY IN BACTERIA.				
THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT				
IS CLAMPED ONTO DNA, IT SLIDES FREELY (BIDIRECTIONAL AND ATP-				
INDEPENDENT) ALONG DUPLEX DNA (BY SIMILARITY).				
+ (DNA) (N).				
-I- CATALYTIC ACTIVITY: N-deoxynucleoside triphosphate = N diphosphate				
+ SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This				
core dimerizes to form the POLIII complex. POLIII associates				
with the gamma complex (composed of gamma, delta', delta, psi and				
chi chains) and with the beta chain to form the complete DNA				
Polymerase III complex (By similarity).				
-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).				
RESULT 8				
F123_CORVE	STANDARD;	PRT;	283 AA.	
ID F123_CORVE				
AC 074631;				
DT 30-MAY-2000 (Rel. 39, Created)				
DT 30-MAY-2000 (Rel. 39, Last sequence update)				
DT 30-MAY-2000 (Rel. 39, Last annotation update)				
DE Protein FDD123 (CtHSP30/1).				
GN FDD123.				
RA Iimura Y., Tatsunari K.				
RA "Isolation of mRNAs induced by a hazardous chemical in white-rot				
fungus, Coriolus versicolor, by differential display";				
RL FBS Lett. 412:370-374 (1997).				
-I- SUBCELLULAR LOCATION: Integral membrane protein (Probable).				
CC -I- SIMILARITY: BELONGS TO THE ARCHAEL OPSIN FAMILY. HSP0				
CC SUBFAMILY.				
CC SEQUENCE FROM N.A.				
CC STRAIN=IFO 30340;				
CC MEDLINE=97398356; PubMed=9256254;				
CC OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;				
CC OC Aphylophorales; Coriolaceae.				
CC OC NCBI_TAXID=37466;				
CC RN [1].				
CC RP SEQUENCE FROM N.A.				
CC RC STRAIN=IFO 30340;				
CC RX MEDLINE=97398356; PubMed=9256254;				
CC RA Iimura Y., Tatsunari K.				
CC RT "Isolation of mRNAs induced by a hazardous chemical in white-rot				
fungus, Coriolus versicolor, by differential display";				
CC RL FBS Lett. 412:370-374 (1997).				
CC CC -I- SIMILARITY: BELONGS TO THE ARCHAEL OPSIN FAMILY. HSP0				
CC CC SEQUENCE FROM N.A.				
CC CC STRAIN=R842HP;				
CC CC MEDLINE=94290261;				
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CC CC [1].				
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CC CC NCBI_TAXID=2133;				
CC CC [1].				
CC CC SEQUENCE FROM N.A.				

Db	243 DYATFGLHSG 252	RN [1] SEQUENCE FROM N.A. RP STRAIN=El Tor N16961 / serotype O1; RC MEDLINE=20046833; PubMed=10952201; RX Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L., ID DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;
RN [1]	SEQUENCE FROM N.A. RP STRAIN=El Tor N16961 / serotype O1; RC MEDLINE=20046833; PubMed=10952201; RX Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L., ID DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;	RN [1] SEQUENCE FROM N.A. RP STRAIN=El Tor N16961 / serotype O1; RC MEDLINE=20046833; PubMed=10952201; RX Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L., ID DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;
RN [1]	SEQUENCE FROM N.A. RP STRAIN=El Tor N16961 / serotype O1; RC MEDLINE=20046833; PubMed=10952201; RX Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L., ID DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;	RN [1] SEQUENCE FROM N.A. RP STRAIN=El Tor N16961 / serotype O1; RC MEDLINE=20046833; PubMed=10952201; RX Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L., ID DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;
RN [1]	SEQUENCE FROM N.A. RP STRAIN=El Tor N16961 / serotype O1; RC MEDLINE=20046833; PubMed=10952201; RX Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L., ID DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;	RN [1] SEQUENCE FROM N.A. RP STRAIN=El Tor N16961 / serotype O1; RC MEDLINE=20046833; PubMed=10952201; RX Heidelberg J.F.; Eisen J.A.; Nelson W.C.; Clayton R.A.; Gwinn M.L., ID DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;
RESULT 9	DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;	RESULT 9 DEKB_STRBQ STANDARD; PRT; 537 AA. AC 059100; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Glucan 1,6-alpha-glucosidase (EC 3.2.1.70) (Dextran glucosidase). DE (EcoR-1,6-alpha-glucosidase) (Glucodextranase). GN DEKB. OS Streptococcus equisimilis. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OC NCBI_TAXID=119602;
RESULT 10	Y690_VIBCH STANDARD; PRT; 307 AA. AC Q9KU39; DT 15-SEP-2003 (Rel. 42, Created) DT 15-SEP-2003 (Rel. 42, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Hypothetical protein YC0690. GN VC0690. OS Vibrio cholerae. OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales; OC Vibrionaceae; Vibrio. OC NCBI_TAXID=666;	RESULT 10 Y690_VIBCH STANDARD; PRT; 307 AA. AC Q9KU39; DT 15-SEP-2003 (Rel. 42, Created) DT 15-SEP-2003 (Rel. 42, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Hypothetical protein YC0690. GN VC0690. OS Vibrio cholerae. OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrios. OC Vibrionaceae; Vibrio. OC NCBI_TAXID=666;

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Z71781; CAA98591.1; -;

EMBL; 274081; CAA98591.1; -;

PAR; S67566; S67566;

SCD; S002191; YDL033C.

InterPro; IPR004506; TrmU.

Pfam; PF0305; tRNA\_Me\_trans; 1.

TIGRFams; TIGR00420; trmU; 1.

Transferase; Methyltransferase; tRNA Processing, tRNA processing, sequence; 417 AA; 47049 MW; 15BF63FD9A094890 CRC64;

Query Match Score 36; DB 1; Length 417;

Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

3 KATFGTHDG 11

1 :|:|||

264 KTWGHDG 272

RESULT 12

PO2678; PDB\_PETMA STANDARD; PRT; 477 AA.

21-JUL-1986 (Rel. 01, Created)

01-OCT-1989 (Rel. 12, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Fibrinopeptide beta chain [Contains: Fibrinopeptide B] (Fragments).

Petromyzon marinus (Sea lamprey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

Petromyzontiformes; Petromyzontidae; Petromyzon.

NCBI\_TaxID=7757;

DR PIR; A25052; A25052;

DR PDB; 1IWW; 23-AUG-02;

DR PDB; 1N73; 07-JAN-03;

DR InterPro; IPR00181; Fibronogen\_C.

SMART; SM00186; FBG; 1.

DR PROSITE; PS00514;

KW Blood coagulation; Fibrin\_Ag\_C\_DOMAIN; 1.

PEPTIDE; Fibrinopeptide B.

FT NON\_CONS 36 37

FT CHAIN <37 477

FT MOD\_RES 13 13

FT CARBONYL 27 27

FT DISULFID 84 84

FT DISULFID 95 95

FT DISULFID 99 99

FT DISULFID 212 212

FT DISULFID 216 216

FT DISULFID 220 304

FT DISULFID 230 259

FT DISULFID 412 425

SEQUENCE 477 AA; 54270 MW; B8A93E7E32D09D1B CRC64;

Query Match Score 36; DB 1; Length 477;

Best Local Similarity 58.1%; Pred. No. 17;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps

QY 1 KDKATFGTHDG 11

DB 442 KEQADYSTDGG 452

SEQUENCE OF 1-36. MEDLINE=77065679; PubMed=999898;  
Cottrell B.A., Doolittle R.F.  
"Amino acid sequences of lamprey fibrinopeptides A and B and  
characterizations of the junctions split by lamprey and mammalian

[2] SEQUENCE OF 37-477 FROM N.A.  
MEDL IND-02076500, DLMV-4-27005-27.

**1** Bohonos V. L., Doolittle R. F., Pontes M., Strong D. D.;  
2 *Biocompatibility* 25(651-652) 1988.  
3 *Biochemistry* 25(651-652) 1988.

-1- FUNCTION: FIBRINogen HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION

-1- SUBUNIT: HEPTAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRIN PEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE

EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT MONOMERS.

-|- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

**EMBL** **outstanding** **collaboration** **between** **the** **Swiss** **Institute** **of** **Bioinformatics** **and** **the** **EMBL** **outstanding** **collaboration** **between** **the** **Swiss** **Institute** **of** **Bioinformatics** **and** **the** **European** **Bioinformatics** **Institute**. **There** **are** **no** **restrictions** **on**

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or send an email to [license@ib-sib.ch](mailto:license@ib-sib.ch).

Brouillet S., Bruschi C.V., Carter N.M., Capuano G., Gardwell B.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Gulisetti G., Guy B.J., Haga K., Haleij J., Harwood C.R., Heineut A., Hilbert H., Hollsapele S., Hosono S., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerz Blanchard M., Klein C., Kobayashi Y., Koeter P., Konigstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Leyne A., Liu H., Masuda S., Manuel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Oudega B., Park S.H., Parro V., Pohl T.M., Portereil D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purcell B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivoira C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schleicher S., Schroeter R., Scoffone F., Sekiguchi J., Sekova A., Seror S.J., Seirori P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takegaki T., Takemaru K., Takeuchi M., Tamakoshi H., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandebol M., Vanmeren F., Vassarotti A., Viari A., Wambutt R., Wedler B., Weitzeneger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshihikawa H., Zumstein E., Yoshihikawa H., Danchin A., Bacillus RT

bt1115 :  
ture 390:249-256(1997).  
- FUNCTION: Autolysins are involved in some important biological processes such as cell separation, cell-wall turnover, competence for genetic transformation, formation of the flagella - in particular of its basal body - and sporulation. Has a high affinity for teichoic acid-endowed peptidoglycan.  
- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl residues and L-amino acid residues in certain bacterial cell-wall glycopeptides.  
- SUBCELLULAR LOCATION: Membrane-bound.  
- SIMILARITY: BELONGS TO THE N-ACETYLGLURAMOYL-L-ALANINE AMIDASE FAMILY 3.

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```

CC EMBL; M8745; AAA22581; 1; -
DR EMBL; M8124; AAA22371; 1; -
DR EMBL; D10388; BAA01225; 1; -
DR EMBL; Z99322; CAB1579; 1; -
PIR; B41322; B1322;
DR SubList; BG10407; lytC.
DR InterPro; IPR002508; Amidase_3.
DR Pfam; PF05120; Amidase_3; 1.
DR Pfam; PF01222; CW_banding_2; 3.
SMART; SM00646; Ami_3; 1.
DR Competence; Sporulation; Hydrolase; Cell wall; Membrane; Repeat;
KW SIGNAL; complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 496 N-ACETYLGLUCOSAMINYL-L-ALANINE AMIDASE CWL8.
FT DOMAIN 30 318 3 X TANDEM REPEATS.
FT REPEAT 30 128 1.
FT REPEAT 129 222 2.
FT REPEAT 223 318 3.
SEQUENCE 496 AA; 52625 MW; 146FF36BA1BB5EC5 CRC64;

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Qy 1 EDKATEFGTHDG 11
      Query Match 58.1%; Score 36; DB 1; Length 496;
      Best Local Similarity 63.6%; Pred. No. 17;
      Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps

```

Db	480	KDKAAQAIHDG	490
	RESULT	14	
	PHSG_BACSU		
	ID PHSG_BACSU	STANDARD;	
	AC P9123;		
	DT 01-FEB-1995	(Rel. 31, Cre	
	DT 01-FEB-1995	(Rel. 31, Las	
	DT 28-FEB-2003	(Rel. 41, Las	
	DE Glycogen phosphorylase (E		
	GN GPC		
	OS Bacillus subtilis.		
	OC Bacteria; Firmicutes; Bac		
	NCBI_TAXID=1423;		
	[1]		
	RN		
	RP SEQUENCE FROM N.A.		
	RC STRAIN=168;		
	RX MEDLINE=94195107;	PubMed	
	RA Klei, J.A.K.W., Boels J.M.		
	RT "Glycogen in Bacillus sub		
	RT operon encoding enzymes /"		
	RT degradation /"		
	RL Microbiology 143:3431-344		
	RN [3]		
	RP SEQUENCE FROM N.A.		
	RC STRAIN=168;		
	RX MEDLINE=98040433;	PubMed	
	RA Kunst F., Ogasawara N., M		
	RA Azevedo V., Bercero M.G.		
	RA Borrius R., Boursier L,		
	RA Brouillet S., Bruschi C.		
	RA Choi S.K., Codani J.J., C		
	RA Denizot F., Devine K.M.,		
	RA Entian K.D., Errington J.		
	RA Fritz C., Fujita M., Fujii		
	RA Ghin S.Y., Glaser P., Go		
	RA Guiseppi G., Guy B.J., He		
	RA Hilpert H., Hollappel C.		
	RA Joris B., Karzai D., Kr		
	RA Kobayashi Y., Koettner P.		
	RA Kurita K., Lapidus A., Le		
	RA Lee S.M., Levine A., Liu		
	RA Medina N., Mellado R.P.,		
	RA Noone D., O'Neill M., Oo		
	RA Parbo V., Pohl T.M., Po		
	RA Presecan E., Pujic P., Pu		
	RA Rieger M., Rivolta C., Ro		
	RA Sato T., Scanlan E., Sc		
	RA Sekiguchi J., Sakowska A		
	RA Sorokin A., Tacconi E.,		
	RA Takemoto K., Tamakoshi A		
	RA Takemoto M., Uchiyama S.,		
	RA Tosato V., Wambat R., We		
	RA Viari A., Wipat A., Wan		
	RA Winters P., Wipat A., Ya		
	RA Yoshida K., Yoshioka H,		
	RT "The complete genome seq		
	RT subline 1,"		
	RX MEDLINE=249-256(1997)		
	Nature 390: 249-256(1997)		

- I - FUNCTION: PHOSPHORYLATION, CARBOHYDRATE METABOLISM, THEIR REGULATORY MECHANISMS; HOWEVER, ALL KNOWN PROPERTIES.

CC ((1,4)-alpha-D-glucosyl) (N-1) + alpha-D-glucose 1-phosphate.  
 CC -I- COFACTOR: Pyridoxal phosphate.  
 CC -I- INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON  
 CC SOURCES THAT ALLOW EFFICIENT SPOORIZATION.  
 CC -I- SIMILARITY: BELONGS TO THE GLYCOSYL PHOSPHORYLASE FAMILY.

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DR EMBL; Z25795; CAA01044.1;  
 DR EMBL; AF008240; AAC00218.1;  
 DR PIR; Z39119; CAB15072.1;  
 DR PIR; S40052; S40052.  
 DR HSSP; P06738; 1YGP.  
 DR SubtilList; BG10911; g1gp.  
 DR InterPro; IPR00811; Glyco\_trans\_35.  
 DR Pfam; PF00343; phosphotransferase; 1.  
 DR PROSITE; PS00102; PHOSPHORYLASE; 1.  
 KW Transferase; Glycosyltransferase; Allosteric enzyme;  
 KW Carbohydrate metabolism; Glycogen metabolism; Pyridoxal phosphate;  
 KW Complete proteome;  
 FT BINDING 646 646 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 798 AA; 91755 MW; 2E5FD08F05C75045 CRC34;

Query Match 58.1%; Score 36; DB 1; Length 798;  
 Best Local Similarity 85.7%; Pred. No. 29;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TFGTHDG 11  
 Db 654 TIGTHDG 660

## RESULT 15

UL/0\_MCMV5 STANDARD: PRT; 964 AA.  
 ID UL70-MCNV5  
 AC 069153;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Helicase/primate complex protein (probable DNA replication protein  
 DE UL70).  
 GN UL70.  
 OS Murine cytomegalovirus (strain Smith).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Marmogalovirus.  
 OC NCBITaxonID=10367;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE-96082764; PubMed=7483291;

RA Messerle M., Rapp M., Lucin P., Kozinowski U.H.;  
 RT Characterization of a conserved gene block in the murine  
 RT cytomegalovirus genome.  
 RL Virus Genes 10:73-80(1995).

CC -I- FUNCTION: INVOLVED IN DNA REPLICATION (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL52.

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DR EMBL; L07319; AAA196665.1;  
 DR InterPro; IPR004340; UL52\_UL70.